# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10 531 543

Source: PCT

Date Processed by STIC: 4-26-05

# *ENTERED*

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/531,543

DATE: 04/26/2005
TIME: 15:48:06

Input Set : A:\PCT-KR2003-002190(Sequence List).txt
Output Set: N:\CRF4\04262005\J531543.raw

```
  1 <110> APPLICANT: SUNGKYUNKWAN UNIVERSITY
  3 <120> TITLE OF INVENTION: Composition for treating virus infection disease comprising
Jab1
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/531,543
C--> 5 <141> CURRENT FILING DATE: 2005-04-15
W--> 0 <130> FILE REFERENCE:
  5 <160> NUMBER OF SEQ ID NOS: 6
  7 <170> SOFTWARE: KopatentIn 1.71
  9 <210> SEQ ID NO: 1
 10 <211> LENGTH: 1262
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Homo sapiens
 14 <220> FEATURE:
 15 <221> NAME/KEY: gene
 16 <222> LOCATION: (1)..(1262)
 17 <223> OTHER INFORMATION: Jab1
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (94)..(1095)
 24 <400> SEQUENCE: 1
 25 ctggtgggga aggtccaaag cccgcacgct gaggcccagt agaagaaagt tgcatcttga          60
 27 ttgtggagcg acagcttctc cggtgcctcg gcc          atg gca gct tcc ggg         108
 28                                              Met Ala Ala Ser Gly
 29                                              1                   5
 31 agt ggt atg gcc cag aaa acc tgg gaa ttg gcc aac aac atg cag gaa          156
 32 Ser Gly Met Ala Gln Lys Thr Trp Glu Leu Ala Asn Asn Met Gln Glu
 33                 10                  15                  20
 35 gcg cag agt atc gat gaa atc tac aaa tat gac aaa aaa caa caa caa          204
 36 Ala Gln Ser Ile Asp Glu Ile Tyr Lys Tyr Asp Lys Lys Gln Gln Gln
 37                 25                  30                  35
 39 gaa atc ctg gcg gcg aaa ccc tgg act aag gat cac cac tac ttt aaa          252
 40 Glu Ile Leu Ala Ala Lys Pro Trp Thr Lys Asp His His Tyr Phe Lys
 41         40                  45                  50
 43 tac tgc aaa atc tca gca ttg gct cta ctg aaa atg gtg atg cat gcc          300
 44 Tyr Cys Lys Ile Ser Ala Leu Ala Leu Leu Lys Met Val Met His Ala
 45         55                  60                  65
 47 agg tca gga ggc aac ttg gaa gtg atg ggt ttg atg ctc ggg aaa gtc          348
 48 Arg Ser Gly Gly Asn Leu Glu Val Met Gly Leu Met Leu Gly Lys Val
 49 70                  75                  80                  85
 51 gac ggc gag acc atg atc atc atg gac agt ttc gct ttg cct gta gag          396
 52 Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe Ala Leu Pro Val Glu
 53                 90                  95                  100
 55 ggc aca gaa act cga gta aat gct caa gct gct gcg tat gag tat atg          444
 56 Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala Ala Tyr Glu Tyr Met
```

```
57              105                   110                .  115
59 gct gca tac ata gaa aat gcc aaa cag gtt ggc cgc ctt gag aat gca        492
60 Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly Arg Leu Glu Asn Ala
61              120                   125                   130
63 atc ggt tgg tat cat agc cac cct ggt tat ggc tgc tgg ctc tcc ggg        540
64 Ile Gly Trp Tyr His Ser His Pro Gly Tyr Gly Cys Trp Leu Ser Gly
65        135                   140                   145
67 att gat gtt agt aca cag atg ctg aac cag cag ttt caa gaa cca ttt        588
68 Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln Phe Gln Glu Pro Phe
69 150                   155                   160                   165
71 gta gca gtg gtg att gat cca acc aga aca atc tct gca gga aaa gtg        636
72 Val Ala Val Val Ile Asp Pro Thr Arg Thr Ile Ser Ala Gly Lys Val
73                   170                   175                   180
75 aat ctt ggc gcc ttt agg aca tat cca aag ggc tac aaa cct cct gat        684
76 Asn Leu Gly Ala Phe Arg Thr Tyr Pro Lys Gly Tyr Lys Pro Pro Asp
77              185                   190                   195
79 gaa gga cct tct gag tac cag act atc cca ctt aat aaa ata gaa gat        732
80 Glu Gly Pro Ser Glu Tyr Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp
81              200                   205                   210
83 ttt ggc gtg cac tgc aaa caa tat tat gcc tta gaa gtc tca tat ttc        780
84 Phe Gly Val His Cys Lys Gln Tyr Tyr Ala Leu Glu Val Ser Tyr Phe
85        215                   220                   225
87 aaa tca tct ttg gat cgt aaa cta ctt gag ctt ttg tgg aat aaa tac        828
88 Lys Ser Ser Leu Asp Arg Lys Leu Leu Glu Leu Leu Trp Asn Lys Tyr
89 230                   235                   240                   245
91 tgg gtg aat acc ctg agt tcc tct agc ttg ctt act aat gca gac tac        876
92 Trp Val Asn Thr Leu Ser Ser Ser Ser Leu Leu Thr Asn Ala Asp Tyr
93                   250                   255                   260
95 acc aca ggc cag gtg ttt gat ttg tct gag aag tta gag cag tcg gaa        924
96 Thr Thr Gly Gln Val Phe Asp Leu Ser Glu Lys Leu Glu Gln Ser Glu
97          265                   270                   275
99 gcc caa ctg gga cgt ggc agt ttc atg ttg ggc tta gaa aca cat gac        972
100 Ala Gln Leu Gly Arg Gly Ser Phe Met Leu Gly Leu Glu Thr His Asp
101              280                   285                   290
103 cgc aag tcg gaa gac aaa ctt gcc aaa gct act aga gac agc tgt aaa       1020
104 Arg Lys Ser Glu Asp Lys Leu Ala Lys Ala Thr Arg Asp Ser Cys Lys
105        295                   300                   305
107 acc acc ata gaa gcc atc cat gga ctg atg tct cag gtt att aag gat       1068
108 Thr Thr Ile Glu Ala Ile His Gly Leu Met Ser Gln Val Ile Lys Asp
109 310                   315                   320                   325
111 aaa ctg ttt aat cag att aac gtt gct    tagtt accaccaagt acttctcaaa    1120
112 Lys Leu Phe Asn Gln Ile Asn Val Ala
113                          330
115 gctggtgtgt ggaaggaaaa gaagctcaag taacactttt aacccagtta ccaaaactca    1180
117 gattagaaga ctaaggtgct gtgtggtgtc ctgagtatta gcactgtaat aaaactatca    1240
119 cgtgaaaaaa aaaaaaaaaa aa                                             1262
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 334
124 <212> TYPE: PRT
```

RAW SEQUENCE LISTING                    DATE: 04/26/2005
PATENT APPLICATION:  US/10/531,543      TIME: 15:48:06

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```
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
128 Met Ala Ala Ser Gly Ser Gly Met Ala Gln Lys Thr Trp Glu Leu Ala
129  1               5                  10                  15
131 Asn Asn Met Gln Glu Ala Gln Ser Ile Asp Glu Ile Tyr Lys Tyr Asp
132             20                  25                  30
134 Lys Lys Gln Gln Gln Glu Ile Leu Ala Ala Lys Pro Trp Thr Lys Asp
135         35                  40                  45
137 His His Tyr Phe Lys Tyr Cys Lys Ile Ser Ala Leu Ala Leu Leu Lys
138         50                  55                  60
140 Met Val Met His Ala Arg Ser Gly Gly Asn Leu Glu Val Met Gly Leu
141  65                  70                  75                  80
143 Met Leu Gly Lys Val Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe
144             85                  90                  95
146 Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala
147             100                 105                 110
149 Ala Tyr Glu Tyr Met Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly
150         115                 120                 125
152 Arg Leu Glu Asn Ala Ile Gly Trp Tyr His Ser His Pro Gly Tyr Gly
153         130                 135                 140
155 Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln
156 145                 150                 155                 160
158 Phe Gln Glu Pro Phe Val Ala Val Val Ile Asp Pro Thr Arg Thr Ile
159             165                 170                 175
161 Ser Ala Gly Lys Val Asn Leu Gly Ala Phe Arg Thr Tyr Pro Lys Gly
162             180                 185                 190
164 Tyr Lys Pro Pro Asp Glu Gly Pro Ser Glu Tyr Gln Thr Ile Pro Leu
165         195                 200                 205
167 Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ala Leu
168         210                 215                 220
170 Glu Val Ser Tyr Phe Lys Ser Ser Leu Asp Arg Lys Leu Leu Glu Leu
171 225                 230                 235                 240
173 Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Ser Leu Leu
174             245                 250                 255
176 Thr Asn Ala Asp Tyr Thr Thr Gly Gln Val Phe Asp Leu Ser Glu Lys
177         260                 265                 270
179 Leu Glu Gln Ser Glu Ala Gln Leu Gly Arg Gly Ser Phe Met Leu Gly
180         275                 280                 285
182 Leu Glu Thr His Asp Arg Lys Ser Glu Asp Lys Leu Ala Lys Ala Thr
183         290                 295                 300
185 Arg Asp Ser Cys Lys Thr Thr Ile Glu Ala Ile His Gly Leu Met Ser
186 305                 310                 315                 320
188 Gln Val Ile Lys Asp Lys Leu Phe Asn Gln Ile Asn Val Ala
189             325                 330
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 32
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
```

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Output Set: **N:\CRF4\04262005\J531543.raw**

```
198 <223> OTHER INFORMATION: primer for WNV-Cp amplification
201 <400> SEQUENCE: 3
202 ccggaattct ctaaaaaacc aggtggcccc gg                          32
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 33
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: primer for WNV-Cp amplification
214 <400> SEQUENCE: 4
215 gactagcggt cgcacccgcg catcgagctc gcc                         33
218 <210> SEQ ID NO: 5
219 <211> LENGTH: 32
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: primer for DNA sequencing
227 <400> SEQUENCE: 5
228 ctattcgatg atgaagatac cccaccaaac cc                          32
231 <210> SEQ ID NO: 6
232 <211> LENGTH: 33
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: primer for DNA sequencing
240 <400> SEQUENCE: 6
241 tagcatctat gactttttgg ggcgttcaag tga                         33
```

**VERIFICATION SUMMARY**                    DATE: 04/26/2005
PATENT APPLICATION:  **US/10/531,543**      TIME: 15:48:07

Input Set : **A:\PCT-KR2003-002190(Sequence List).txt**
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L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE